

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 09/926,323 B  
Source: IFW16  
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IFW16

## RAW SEQUENCE LISTING

DATE: 09/22/2005

PATENT APPLICATION: US/09/926,323B

TIME: 14:52:36

Input Set : A:\2923-508.txt

Output Set: N:\CRF4\09222005\I926323B.raw

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3 <110> APPLICANT: Schmitt, Manfred
4      Noack, Frank
5      Magdolen, Viktor
6      Graeff, Henner
7      Luther, Thomas
8      Albrecht, Sybille
9      Muller, Martin
10     Wilhelm, Olaf
11     Harbeck, Nadia
13 <120> TITLE OF INVENTION: Diagnostic and Therapeutic Use of Antibodies Against The
14     Urokinase Receptor
16 <130> FILE REFERENCE: 2923-508
18 <140> CURRENT APPLICATION NUMBER: US 09/926,323B
19 <141> CURRENT FILING DATE: 2002-03-05
21 <150> PRIOR APPLICATION NUMBER: PCT/EP00/03347
22 <151> PRIOR FILING DATE: 2000-04-13
24 <150> PRIOR APPLICATION NUMBER: EP 99107199.4
25 <151> PRIOR FILING DATE: 1999-04-13
27 <160> NUMBER OF SEQ ID NOS: 10
29 <170> SOFTWARE: PatentIn version 3.2
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 354
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: phage sequence
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)..(354)
44 <400> SEQUENCE: 1
45 cag gtg caa ctg cag cag tca gga cct gag ttg gtg aag cct ggg gct      48
46 Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
47 1          5          10          15
49 tta gtg aag ata tcc tgc aag gct tct ggt tac agt ttc aca agc tac      96
50 Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
51          20          25          30
53 gat ata aat tgg gtg aag cgg agg cct gga cag gga ctt gag tgg att      144
54 Asp Ile Asn Trp Val Lys Arg Arg Pro Gly Gln Gly Leu Glu Trp Ile
55          35          40          45
57 gga tgg att ttt cct gga gat ggt agt acc aat tac aat gag aaa ttc      192
58 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Asn Tyr Asn Glu Lys Phe
59          50          55          60
61 aag gac aag gcc aca ctg act gct gac aaa tcc tcc agc aca gcc tac      240

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62 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
63 65          70          75          80
65 atg cag ctc aac agc ctg act tct gag aac tct gca gtc tat ttc tgt      288
66 Met Gln Leu Asn Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
67          85          90          95
69 gca aga gat gga agt atg ggg ggg ttt gac tac tgg ggc caa ggg acc      336
70 Ala Arg Asp Gly Ser Met Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
71          100          105          110
73 acg gtc acc gtc tcc tca      354
74 Thr Val Thr Val Ser Ser
75          115
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 118
80 <212> TYPE: PRT
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: phage sequence
86 <400> SEQUENCE: 2
88 Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
89 1          5          10          15
92 Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
93          20          25          30
96 Asp Ile Asn Trp Val Lys Arg Arg Pro Gly Gln Gly Leu Glu Trp Ile
97          35          40          45
100 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Asn Tyr Asn Glu Lys Phe
101          50          55          60
104 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
105 65          70          75          80
108 Met Gln Leu Asn Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
109          85          90          95
112 Ala Arg Asp Gly Ser Met Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
113          100          105          110
116 Thr Val Thr Val Ser Ser
117          115
120 <210> SEQ ID NO: 3
121 <211> LENGTH: 324
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: phage sequence
129 <220> FEATURE:
130 <221> NAME/KEY: CDS
131 <222> LOCATION: (1)..(324)
133 <400> SEQUENCE: 3
134 gat gtt ttg atg acc caa act cca aaa ttc atg tcc aca tca gta gga      48
135 Asp Val Leu Met Thr Gln Thr Pro Lys Phe Met Ser Thr Ser Val Gly
136 1          5          10          15
138 gac agg gtc agc atc acc tgc aag gcc agt cag aat gtt cgt act act      96
139 Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Arg Thr Thr

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140          20          25          30
142 gta gcc tgg tat caa gag aaa cca ggg cag tct cct aaa gca ctg att      144
143 Val Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
144          35          40          45
146 tac ttg gca tcc aac cgg cac act gga gtc cct gat cgc ttc aca ggc      192
147 Tyr Leu Ala Ser Asn Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
148          50          55          60
150 agt gga tct gga aca gat ttc act ctc acc att agc aat gtg caa tct      240
151 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
152 65          70          75          80
154 gaa gac ctg gca gat tat ttc tgt ctg caa cat tgg aat tat ccg tac      288
155 Glu Asp Leu Ala Asp Tyr Phe Cys Leu Gln His Trp Asn Tyr Pro Tyr
156          85          90          95
158 acg ttc gga ggg ggc acc aag ctg gaa atc aaa cgg      324
159 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
160          100          105
163 <210> SEQ ID NO: 4
164 <211> LENGTH: 108
165 <212> TYPE: PRT
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: phage sequence
171 <400> SEQUENCE: 4
173 Asp Val Leu Met Thr Gln Thr Pro Lys Phe Met Ser Thr Ser Val Gly
174 1          5          10          15
177 Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Arg Thr Thr
178          20          25          30
181 Val Ala Trp Tyr Gln Glu Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
182          35          40          45
185 Tyr Leu Ala Ser Asn Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
186          50          55          60
189 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
190 65          70          75          80
193 Glu Asp Leu Ala Asp Tyr Phe Cys Leu Gln His Trp Asn Tyr Pro Tyr
194          85          90          95
197 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
198          100          105
201 <210> SEQ ID NO: 5
202 <211> LENGTH: 9
203 <212> TYPE: PRT
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: CDR3-VH sequence
209 <400> SEQUENCE: 5
211 Asp Gly Ser Met Gly Gly Phe Asp Tyr
212 1          5
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 9
217 <212> TYPE: PRT

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218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: CDR3-LH sequence
223 <400> SEQUENCE: 6
225 Leu Gln His Trp Asn Tyr Pro Tyr Thr
226 1 5
229 <210> SEQ ID NO: 7
230 <211> LENGTH: 5
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: CDR1-VH sequence
237 <400> SEQUENCE: 7
239 Ser Tyr Asp Ile Asn
240 1 5
243 <210> SEQ ID NO: 8
244 <211> LENGTH: 11
245 <212> TYPE: PRT
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: CDR1-VL sequence
251 <400> SEQUENCE: 8
253 Lys Ala Ser Gln Asn Val Arg Thr Thr Val Ala
254 1 5 10
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259 <212> TYPE: PRT
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262 <220> FEATURE:
263 <223> OTHER INFORMATION: CDR2-VH sequence
265 <400> SEQUENCE: 9
267 Trp Ile Phe Pro Gly Asp Gly Ser Thr Asn Tyr Asn Glu Lys Phe Lys
268 1 5 10 15
271 Asp
275 <210> SEQ ID NO: 10
276 <211> LENGTH: 7
277 <212> TYPE: PRT
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: CDR2-VL sequence
283 <400> SEQUENCE: 10
285 Leu Ala Ser Asn Arg His Thr
286 1 5

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**VERIFICATION SUMMARY**

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